

PATENT  
USSN 10/054,611  
Docket 002970US; 018/182c

### CLAIM AMENDMENTS

1. *(Currently Amended)* A method of identifying a nucleic acid in a sample, comprising:
  - a) combining the sample with a polynucleotide probe ~~comprising a sequence identical or complementary to at least 10 consecutive nucleotides contained in SEQ ID NO:224~~, such that the probe hybridizes specifically to the nucleic acid if the nucleic acid encodes human telomerase reverse transcriptase (hTERT) or fragment thereof;
  - b) detecting any hybrid formed as a result of a); and
  - c) identifying the nucleic acid as encoding ~~at least a portion of human telomerase reverse transcriptase (hTERT)~~ hTERT or fragment thereof if the hybrid is detected;  
wherein the probe hybridizes specifically to a DNA having the sequence of the hTERT encoding region of SEQ. ID NO:224 at 5°C to 25°C below  $T_m$  in aqueous solution at 1 M NaCl;  
wherein  $T_m$  is the melting temperature of double-stranded DNA having the sequence of said encoding region under the same reaction conditions.
2. *(Currently Amended)* A method of detecting a nucleic acid that encodes hTERT or fragment thereof in a sample, comprising:
  - a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO:224 if present in the sample; and
  - b) detecting any hybrid formed as a result of a);  
wherein the polynucleotide probe ~~comprises~~ consists essentially of a sequence identical or complementary to at least 25 or more consecutive nucleotides contained in from the hTERT encoding region of SEQ ID NO:224.
3. *(Original)* The method of claim 2, wherein the hTERT nucleic acid is human genomic DNA.
4. *(Currently Amended)* The method of claim 2, wherein the hTERT nucleic acid is human mRNA or cDNA.
5. *(Currently Amended)* The method of claim 2, wherein the hTERT nucleic acid comprises at least 250 or more nucleotides of SEQ ID NO:224.
6. *(Currently Amended)* The method of claim 2, wherein the hTERT nucleic acid comprises at least 500 or more nucleotides of SEQ ID NO:224.

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7. *(Currently Amended)* The method of claim 2, wherein the probe comprises a sequence identical or complementary to at least 30 or more consecutive nucleotides contained in from the hTERT encoding region of SEQ ID NO:224.
8. *(Currently Amended)* The method of claim 2, wherein the probe comprises a sequence identical or complementary to at least 50 or more consecutive nucleotides contained in from the hTERT encoding region of SEQ ID NO:224.
9. *(Currently Amended)* The method of claim 2, wherein the probe comprises a sequence identical or complementary to at least 100 or more consecutive nucleotides contained in from the hTERT encoding region of SEQ ID NO:224.
10. *(Original)* The method of claim 2, wherein the probe comprises a sequence not contained in SEQ. ID NO:62.
11. *(Original)* The method of claim 9, wherein the probe comprises a sequence not contained in SEQ. ID NO:62.
12. *(Original)* The method of claim 2, wherein the sample is a human biological sample.
13. *(Currently Amended)* A method of identifying a nucleic acid in a sample, comprising:
  - a) combining the sample with a polynucleotide primer ~~containing a sequence identical or complementary to at least 10 consecutive nucleotides contained in SEQ ID NO:224,~~ under conditions that the primer amplifies specifically primes amplification of the nucleic acid if the nucleic acid encodes human telomerase reverse transcriptase (hTERT) or fragment thereof;
  - b) detecting any amplification product formed as a result of a); and
  - c) identifying the nucleic acid as encoding ~~at least a portion of hTERT or fragment thereof~~ if the amplification product is detected;  
wherein the primer hybridizes specifically to a DNA having the sequence of the hTERT encoding region of SEQ. ID NO:224 at 5°C to 25°C below  $T_m$  in aqueous solution at 1 M NaCl;  
wherein  $T_m$  is the melting temperature of double-stranded DNA having the sequence of said encoding region under the same reaction conditions.

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14. *(Currently Amended)* A method of detecting a nucleic acid encoding ~~at least a portion of~~ hTERT ~~or fragment thereof~~ in a sample, comprising:
- a) combining the sample with ~~a polynucleotide primer such that the primer amplifies polynucleotide primers so as to prime amplification of~~ nucleic acid encoding ~~at least a portion of~~ hTERT ~~or fragment thereof~~ if present in the sample; and
  - b) detecting any amplified product formed as a result of a);
- wherein the ~~polynucleotide primer comprises~~ each of said primers consists essentially of a sequence identical or complementary to at least 15 or more consecutive nucleotides contained in from the hTERT encoding region of SEQ ID NO:224.
15. *(Currently Amended)* The method of claim 14, wherein ~~the polynucleotide primer comprises each of said primers consists essentially of~~ a sequence identical or complementary to at least 30 or more consecutive nucleotides ~~contained in from the hTERT encoding region of~~ SEQ ID NO:224.
16. *(Currently Amended)* The method of claim 14, wherein ~~the polynucleotide primer comprises each of said primers consists essentially of~~ a sequence identical or complementary to at least 50 or more consecutive nucleotides ~~contained in from the hTERT encoding region of~~ SEQ ID NO:224.
17. *(Original)* The method of claim 14, wherein the sample is a human biological sample.
18. *(Original)* The method of claim 14, wherein the sample comprises human genomic DNA.
19. *(Currently Amended)* The method of claim 14, wherein the sample comprises ~~human mRNA~~ hTERT mRNA or cDNA.
20. CANCELLED.
21. *(Original)* The method of claim 14, wherein the ~~primer comprises~~ primers comprise a sequence not contained in SEQ. ID NO:62.
22. CANCELLED

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23. (Withdrawn) (Currently Amended) A combination of oligonucleotide primers for PCR amplification for use in detecting an hTERT nucleic acid according to claim 14, comprising a first primer that hybridizes to a polynucleotide consisting of SEQ ID NO:224 under stringent amplification conditions, and a second primer that hybridizes to the complement of said nucleic acid under stringent amplification conditions wherein each primer consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.
24. (Withdrawn) The combination of primers of claim 23, wherein either each primer comprises between consists of 15-30 nucleotides.
25. (Withdrawn) The combination of primers of claim 23, wherein either each primer comprises between consists of 20-25 nucleotides.
26. (Withdrawn) The combination of primers of claim 23, wherein 50% or more of the nucleotides of either each primer are guanine and/or cytosine.
27. (Withdrawn) (Currently Amended) A PCR product that hybridizes under stringent conditions to a polynucleotide having a sequence consisting of formed while undertaking the detection method of claim 14, comprising 15 or more contiguous nucleotides of the hTERT encoding region of SEQ ID NO:224 or its complement.
28. (Withdrawn) (Currently Amended) A hybridization complex formed while undertaking the detection method of claim 2, comprising:  
a) one strand of a cellular hTERT nucleic acid; and  
b) one strand of a nucleic acid comprising a recombinant or synthetic fragment of hTERT, wherein said fragment of hTERT comprises at least 10 contiguous nucleotides of consisting essentially of 25 or more consecutive nucleotides of the hTERT encoding region of SEQ ID NO:224 or its complement.
29. (Withdrawn) The hybridization complex of claim 28, wherein the hTERT nucleic acid is an hTERT mRNA.
30. (Withdrawn) The hybridization complex of claim 28, wherein the hTERT nucleic acid is an hTERT cDNA.
31. (Withdrawn) The hybridization complex of claim 28, wherein the fragment comprises at least 20 contiguous or more consecutive nucleotides of SEQ ID NO:224 or its complement.

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32. *(Withdrawn) (Currently Amended)* The hybridization complex of claim 28, wherein the fragment comprises ~~10-100 contiguous~~ 100 or more consecutive nucleotides of SEQ ID NO:224 or its complement.
33. *(Withdrawn)* The hybridization complex of claim 28, wherein said hybridization complex is a DNA:DNA complex.
34. *(Withdrawn)* The hybridization complex of claim 28, wherein said hybridization complex is a DNA:RNA complex.
35. *(New)* The method of claim 1, wherein a) comprises combining the sample with the probe at 5°C to 25°C below  $T_m$  in aqueous solution at 1 M NaCl.
36. *(New)* The method of claim 1, wherein the hTERT nucleic acid is hTERT mRNA or cDNA.
37. *(New)* The method of claim 1, wherein the probe comprises a sequence identical or complementary to 100 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.
38. *(New)* The method of claim 1, wherein the probe comprises a sequence not contained in SEQ. ID NO:62.
39. *(New)* The method of claim 1, wherein the sample has been taken from a patient, and the method further comprises determining or assessing a tumor in the patient according to whether a nucleic acid encoding hTERT or an hTERT fragment is detected.
40. *(New)* The method of claim 2, wherein the sample has been taken from a patient, and the method further comprises determining or assessing a tumor in the patient according to whether said nucleic acid hybrid is detected.
41. *(New)* The method of claim 13, wherein a) comprises combining the sample with the primer at 5°C to 25°C below  $T_m$  in aqueous solution at 1 M NaCl.
42. *(New)* The method of claim 13, wherein the hTERT nucleic acid is mRNA or cDNA.

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43. *(New)* The method of claim 13, wherein the primer comprises a sequence identical or complementary to 30 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.
44. *(New)* The method of claim 13, wherein the primer comprises a sequence not contained in SEQ. ID NO:62.
45. *(New)* The method of claim 13, wherein the sample has been taken from a patient, and the method comprises determining or assessing a tumor in the patient according to whether a nucleic acid encoding hTERT or an hTERT fragment is detected.
46. *(New)* The method of claim 14, wherein the sample has been taken from a patient, and the method comprises determining or assessing a tumor in the patient according to whether said amplification product is formed.